



SEQUENCE LISTING

<110> Matsui, Ikuo
Horikawa, Kazuhiko
Ishida, Hiroyasu
Kosugi, Yoshitsugu

<120> THERMOPHILIC ENZYMES HAVING
BETA-GLYCOSIDASE ACTIVITY

<130> 11059/002001

<140> 09/369,735

<141> 1999-08-06

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1269

<212> DNA

<213> Pyrococcus horikoshii

<220>

<221> CDS

<222> (1)...(1269)

<400> 1

atg ccg ctg aaa ttc ccg gaa atg ttt ctc ttt ggt acc gca aca tca	48
Met Pro Leu Lys Phe Pro Glu Met Phe Leu Phe Gly Thr Ala Thr Ser	
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tcc cat cag ata gag gga aat aat aga tgg aat gat tgg tgg tac tat	96
Ser His Gln Ile Glu Gly Asn Asn Arg Trp Asn Asp Trp Trp Tyr Tyr	
20 25 30	

gag cag att gga aag ctc ccc tac aga tct ggt aag gct tgc aat cac	144
Glu Gln Ile Gly Lys Leu Pro Tyr Arg Ser Gly Lys Ala Cys Asn His	
35 40 45	

tgg gaa ctt tac agg gat gat att cag cta atg acc agc ttg ggc tat	192
Trp Glu Leu Tyr Arg Asp Asp Ile Gln Leu Met Thr Ser Leu Gly Tyr	
50 55 60	

aat gct tat agg ttc tcc ata gag tgg agc agg cta ttc cca gag gaa	240
Asn Ala Tyr Arg Phe Ser Ile Glu Trp Ser Arg Leu Phe Pro Glu Glu	
65 70 75 80	

aat aaa ttt aat gaa gat gct ttc atg aaa tac cgg gag att ata gac	288
Asn Lys Phe Asn Glu Asp Ala Phe Met Lys Tyr Arg Glu Ile Ile Asp	
85 90 95	

ttg tta ttg acg aga ggt ata act ccc ctg gtg acc cta cac cac ttt	336
Leu Leu Leu Thr Arg Gly Ile Thr Pro Leu Val Thr Leu His His Phe	
100 105 110	

act agc cct ctc tgg ttc atg aag aaa ggt ggc ttc ctt agg gag gag	384
Thr Ser Pro Leu Trp Phe Met Lys Lys Gly Gly Phe Leu Arg Glu Glu	
115 120 125	

aac cta aaa cat tgg gaa aag tac ata gaa aag gtt gct gag ctt tta	432
Asn Leu Lys His Trp Glu Lys Tyr Ile Glu Lys Val Ala Glu Leu Leu	
130 135 140	
gaa aaa gtt aaa cta gta gct acc ttc aat gag ccg atg gta tac gta	480
Glu Lys Val Lys Leu Val Ala Thr Phe Asn Glu Pro Met Val Tyr Val	
145 150 155 160	
atg atg gga tat cta acg gct tat tgg ccc cca ttc att agg agt cca	528
Met Met Gly Tyr Leu Thr Ala Tyr Trp Pro Pro Phe Ile Arg Ser Pro	
165 170 175	
ttt aag gcc ttt aag gta gct gca aac ctg ctt aaa gct cac gca att	576
Phe Lys Ala Phe Lys Val Ala Ala Asn Leu Leu Lys Ala His Ala Ile	
180 185 190	
gcc tat gaa ctt ctt cat ggg aaa ttc aaa gtt gga atc gta aag aat	624
Ala Tyr Glu Leu Leu His Gly Lys Phe Lys Val Gly Ile Val Lys Asn	
195 200 205	
att ccc ata ata ctc cca gcg agt gac aag gag agg gat aga aaa gcc	672
Ile Pro Ile Ile Leu Pro Ala Ser Asp Lys Glu Arg Asp Arg Lys Ala	
210 215 220	
gct gag aaa gct gat aat tta ttt aac tgg cac ttt ttg gat gcg ata	720
Ala Glu Lys Ala Asp Asn Leu Phe Asn Trp His Phe Leu Asp Ala Ile	
225 230 235 240	
tgg agt ggg aaa tac aga ggg gta ttt aaa aca tat agg att ccc caa	768
Trp Ser Gly Lys Tyr Arg Gly Val Phe Lys Thr Tyr Arg Ile Pro Gln	
245 250 255	
agt gac gca gat ttc att ggg gtt aac tat tac acg gcc agc gaa gta	816
Ser Asp Ala Asp Phe Ile Gly Val Asn Tyr Tyr Thr Ala Ser Glu Val	
260 265 270	
agg cat act tgg aat cct tta aaa ttc ttc ttt gag gtg aaa tta gcg	864
Arg His Thr Trp Asn Pro Leu Lys Phe Phe Phe Glu Val Lys Leu Ala	
275 280 285	
gat att agc gag agg aag act caa atg gga tgg agc gtt tat cca aaa	912
Asp Ile Ser Glu Arg Lys Thr Gln Met Gly Trp Ser Val Tyr Pro Lys	
290 295 300	
gga ata tac atg gcc ctt aaa aaa gct tcc agg tat gga agg cct ctt	960
Gly Ile Tyr Met Ala Leu Lys Lys Ala Ser Arg Tyr Gly Arg Pro Leu	
305 310 315 320	
tat att acg gaa aac gga ata gcg acg ctt gat gat gaa tgg aga gtg	1008
Tyr Ile Thr Glu Asn Gly Ile Ala Thr Leu Asp Asp Glu Trp Arg Val	
325 330 335	
gaa ttc ata att caa cac ctc caa tac gtt cat aag gct atc gaa gac	1056
Glu Phe Ile Ile Gln His Leu Gln Tyr Val His Lys Ala Ile Glu Asp	
340 345 350	
ggc ctg gat gta aga ggt tac ttc tat tgg tca ttt atg gat aac tac	1104
Gly Leu Asp Val Arg Gly Tyr Phe Tyr Trp Ser Phe Met Asp Asn Tyr	
355 360 365	

gag tgg aaa gag ggg ttt ggg cct aga ttt ggc cta gtg gaa gtt gat	1152
Glu Trp Lys Glu Gly Phe Gly Pro Arg Phe Gly Leu Val Glu Val Asp	
370 375 380	
tat caa acc ttc gag aga agg ccc agg aag agt gct tac gta tac gga	1200
Tyr Gln Thr Phe Glu Arg Arg Pro Arg Lys Ser Ala Tyr Val Tyr Gly	
385 390 395 400	
gaa att gca aga agt aag gaa ata aag gat gag cta tta aag aga tat	1248
Glu Ile Ala Arg Ser Lys Glu Ile Lys Asp Glu Leu Leu Lys Arg Tyr	
405 410 415	
ggc cta cca gaa ctt caa ctt	1269
Gly Leu Pro Glu Leu Gln Leu	
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<210> 2

<211> 423

<212> PRT

<213> *Pyrococcus horikoshii*

<400> 2

Met Pro Leu Lys Phe Pro Glu Met Phe Leu Phe Gly Thr Ala Thr Ser	
1 5 10 15	
Ser His Gln Ile Glu Gly Asn Asn Arg Trp Asn Asp Trp Trp Tyr Tyr	
20 25 30	
Glu Gln Ile Gly Lys Leu Pro Tyr Arg Ser Gly Lys Ala Cys Asn His	
35 40 45	
Trp Glu Leu Tyr Arg Asp Asp Ile Gln Leu Met Thr Ser Leu Gly Tyr	
50 55 60	
Asn Ala Tyr Arg Phe Ser Ile Glu Trp Ser Arg Leu Phe Pro Glu Glu	
65 70 75 80	
Asn Lys Phe Asn Glu Asp Ala Phe Met Lys Tyr Arg Glu Ile Ile Asp	
85 90 95	
Leu Leu Leu Thr Arg Gly Ile Thr Pro Leu Val Thr Leu His His Phe	
100 105 110	
Thr Ser Pro Leu Trp Phe Met Lys Lys Gly Gly Phe Leu Arg Glu Glu	
115 120 125	
Asn Leu Lys His Trp Glu Lys Tyr Ile Glu Lys Val Ala Glu Leu Leu	
130 135 140	
Glu Lys Val Lys Leu Val Ala Thr Phe Asn Glu Pro Met Val Tyr Val	
145 150 155 160	
Met Met Gly Tyr Leu Thr Ala Tyr Trp Pro Pro Phe Ile Arg Ser Pro	
165 170 175	
Phe Lys Ala Phe Lys Val Ala Ala Asn Leu Leu Lys Ala His Ala Ile	
180 185 190	
Ala Tyr Glu Leu Leu His Gly Lys Phe Lys Val Gly Ile Val Lys Asn	
195 200 205	
Ile Pro Ile Ile Leu Pro Ala Ser Asp Lys Glu Arg Asp Arg Lys Ala	
210 215 220	
Ala Glu Lys Ala Asp Asn Leu Phe Asn Trp His Phe Leu Asp Ala Ile	
225 230 235 240	
Trp Ser Gly Lys Tyr Arg Gly Val Phe Lys Thr Tyr Arg Ile Pro Gln	
245 250 255	
Ser Asp Ala Asp Phe Ile Gly Val Asn Tyr Tyr Thr Ala Ser Glu Val	
260 265 270	
Arg His Thr Trp Asn Pro Leu Lys Phe Phe Phe Glu Val Lys Leu Ala	
275 280 285	
Asp Ile Ser Glu Arg Lys Thr Gln Met Gly Trp Ser Val Tyr Pro Lys	
290 295 300	

Gly Ile Tyr Met Ala Leu Lys Lys Ala Ser Arg Tyr Gly Arg Pro Leu
 305 310 315 320
 Tyr Ile Thr Glu Asn Gly Ile Ala Thr Leu Asp Asp Glu Trp Arg Val
 325 330 335
 Glu Phe Ile Ile Gln His Leu Gln Tyr Val His Lys Ala Ile Glu Asp
 340 345 350
 Gly Leu Asp Val Arg Gly Tyr Phe Tyr Trp Ser Phe Met Asp Asn Tyr
 355 360 365
 Glu Trp Lys Glu Gly Phe Gly Pro Arg Phe Gly Leu Val Glu Val Asp
 370 375 380
 Tyr Gln Thr Phe Glu Arg Arg Pro Arg Lys Ser Ala Tyr Val Tyr Gly
 385 390 395 400
 Glu Ile Ala Arg Ser Lys Glu Ile Lys Asp Glu Leu Leu Lys Arg Tyr
 405 410 415
 Gly Leu Pro Glu Leu Gln Leu
 420

<210> 3

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> An upper primer designed to create the NdeI site.

<400> 3

taagaaggag atatacatat gccgctgaaa ttcccggaaa tgtttctctt tgggtacc

57

<210> 4

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> A lower primer designed to create the BamHI site.

<400> 4

tttactgcag agaggatccc taatcctaaa gttgaagttc tggtag

46

<210> 5

<211> 483

<212> PRT

<213> Pyrococcus horikoshii

<400> 5

Met Lys Phe Tyr Trp Gly Val Val Gln Ser Ala Phe Gln Phe Glu Met
 1 5 10 15
 Gly Asp Pro Tyr Arg Arg Asn Ile Asp Pro Arg Ser Asp Trp Trp Tyr
 20 25 30
 Trp Val Arg Asp Pro Tyr Asn Ile Lys Asn Asp Leu Val Ser Gly Asp
 35 40 45
 Leu Pro Glu Glu Gly Ile Asn Asn Tyr Glu Leu Tyr Glu Ile Asp His
 50 55 60
 Arg Leu Ala Lys Glu Leu Gly Leu Asn Ala Tyr Gln Leu Thr Ile Glu
 65 70 75 80
 Trp Ser Arg Ile Phe Pro Cys Pro Thr Phe Asn Val Glu Val Glu Phe
 85 90 95
 Glu Arg Asp Asx Tyr Gly Leu Ile Lys Lys Val Lys Ile Glu Lys Glu
 100 105 110
 His Leu Glu Glu Leu Asp Lys Leu Ala Asn Gln Lys Glu Val Arg His
 115 120 125

Tyr Leu Asn Val Leu Arg Asn Leu Lys Lys Leu Gly Phe Thr Thr Phe
 130 135 140
 Val Thr Leu Asn His Gln Thr Asn Pro Ile Trp Ile His Asp Pro Ile
 145 150 155 160
 Glu Thr Arg Gly Asn Phe Gln Lys Ala Arg Ala Pro Gly Trp Val Asp
 165 170 175
 Glu Arg Thr Ile Ile Glu Phe Ala Lys Tyr Ala Ala Tyr Val Ala Trp
 180 185 190
 Lys Phe Asp Asn Tyr Val Asp Tyr Trp Ser Thr Phe Asp Glu Pro Met
 195 200 205
 Val Thr Ala Glu Leu Gly Tyr Leu Ala Pro Tyr Val Gly Trp Pro Pro
 210 215 220
 Gly Ile Leu Asn Pro Ser Ala Ala Lys Lys Val Ile Ile Asn Gln Ile
 225 230 235 240
 Val Ala His Ala Pro Ala Tyr Asp Ser Ile Lys Lys Phe Ser Ser Lys
 245 250 255
 Pro Val Gly Val Ile Leu Asn Ile Ile Pro Ala Tyr Pro Leu Asp Pro
 260 265 270
 Asn Asp Ser Lys Ser Val Arg Ala Ala Glu Asn Tyr Asp Leu Phe His
 275 280 285
 Asn Arg Leu Phe Leu Glu Ala Val Asn Arg Gly Asn Val Asp Leu Asp
 290 295 300
 Ile Thr Gly Glu Tyr Thr Lys Ile Pro His Ile Lys Arg Asn Asp Trp
 305 310 315 320
 Ile Gly Asn Asn Tyr Tyr Thr Arg Glu Val Val Lys Tyr Val Glu Pro
 325 330 335
 Lys Tyr Glu Glu Leu Pro Leu Ile Thr Phe Val Gly Val Glu Gly Tyr
 340 345 350
 Gly Tyr Ser Gly Asn Pro Asn Ser Leu Ser Pro Asp Asn Asn Pro Thr
 355 360 365
 Ser Asp Phe Gly Trp Glu Val Phe Pro Gln Gly Leu Tyr Asp Ser Thr
 370 375 380
 Leu Glu Ala Ala Glu Tyr Asn Lys Glu Val Phe Ile Thr Glu Asn Gly
 385 390 395 400
 Ile Ala Asp Ser Lys Asp Ile Leu Arg Pro Arg Tyr Ile Ile Asp His
 405 410 415
 Val Asn Glu Val Lys Lys Leu Ile Glu Asn Gly Ile Lys Val Gly Gly
 420 425 430
 Tyr Phe His Trp Ala Leu Thr Asp Asn Tyr Glu Trp Ala Met Gly Phe
 435 440 445
 Lys Ile Arg Phe Gly Leu Tyr Glu Val Asp Leu Ile Thr Lys Glu Arg
 450 455 460
 Ile Pro Arg Arg Arg Ser Val Glu Ile Tyr Lys Lys Ile Val Met Glu
 465 470 475 480
 Gly Ile Glu

<210> 6

<211> 510

<212> PRT

<213> *Pyrococcus furiosus*

<400> 6

Met Phe Pro Glu Met Phe Leu Trp Gly Val Ala Gln Ser Gly Phe Gln
 1 5 10 15
 Phe Glu Met Gly Asp Lys Leu Arg Arg Asn Ile Asp Thr Asn Thr Asp
 20 25 30
 Trp Trp His Trp Val Arg Asp Lys Thr Asn Ile Glu Lys Gly Leu Val
 35 40 45
 Ser Gly Asp Leu Pro Glu Glu Gly Ile Asn Asn Tyr Glu Leu Tyr Glu
 50 55 60

Lys	Asp	His	Glu	Ile	Ala	Arg	Lys	Leu	Gly	Leu	Asn	Ala	Tyr	Arg	Ile	65	70	75	80
Gly	Ile	Glu	Trp	Ser	Arg	Ile	Phe	Pro	Trp	Pro	Thr	Thr	Phe	Ile	Asp	85	90	95	
Val	Asp	Tyr	Ser	Tyr	Asn	Glu	Ser	Tyr	Asn	Leu	Ile	Glu	Asp	Val	Lys	100	105	110	
Ile	Thr	Lys	Asp	Thr	Leu	Glu	Glu	Leu	Asp	Glu	Ile	Ala	Asn	Lys	Arg	115	120	125	
Glu	Val	Ala	Tyr	Tyr	Arg	Ser	Val	Ile	Asn	Ser	Leu	Arg	Ser	Lys	Gly	130	135	140	
Phe	Lys	Val	Ile	Val	Asn	Leu	Asn	His	Phe	Thr	Leu	Pro	Tyr	Trp	Asp	145	150	155	160
His	Asp	Pro	Ile	Glu	Ala	Arg	Glu	Arg	Ala	Leu	Thr	Asn	Lys	Arg	Asn	165	170	175	
Gly	Trp	Val	Asn	Pro	Arg	Thr	Val	Ile	Glu	Phe	Ala	Lys	Tyr	Ala	Ala	180	185	190	
Tyr	Ile	Ala	Tyr	Lys	Phe	Gly	Asp	Ile	Val	Asp	Met	Trp	Ser	Thr	Phe	195	200	205	
Asn	Glu	Pro	Met	Val	Val	Val	Glu	Leu	Gly	Tyr	Leu	Ala	Pro	Tyr	Ser	210	215	220	
Gly	Phe	Pro	Pro	Gly	Val	Leu	Asn	Pro	Glu	Ala	Ala	Lys	Leu	Ala	Ile	225	230	235	240
Leu	His	Met	Ile	Asn	Ala	His	Ala	Leu	Ala	Tyr	Arg	Gln	Ile	Lys	Lys	245	250	255	
Phe	Asp	Thr	Glu	Lys	Ala	Asp	Lys	Asp	Ser	Lys	Glu	Pro	Ala	Glu	Val	260	265	270	
Gly	Ile	Ile	Tyr	Asn	Asn	Ile	Gly	Val	Ala	Tyr	Pro	Lys	Asp	Pro	Asn	275	280	285	
Asp	Ser	Lys	Asp	Val	Lys	Ala	Ala	Glu	Asn	Asp	Asn	Phe	Phe	His	Ser	290	295	300	
Gly	Leu	Phe	Phe	Glu	Ala	Ile	His	Lys	Gly	Lys	Leu	Asn	Ile	Glu	Phe	305	310	315	320
Asp	Gly	Glu	Thr	Phe	Ile	Asp	Ala	Pro	Tyr	Leu	Lys	Gly	Asn	Asp	Trp	325	330	335	
Ile	Gly	Met	Asn	Tyr	Tyr	Thr	Arg	Glu	Val	Val	Thr	Tyr	Gln	Glu	Pro	340	345	350	
Met	Phe	Pro	Ser	Ile	Pro	Leu	Ile	Thr	Phe	Lys	Gly	Val	Gln	Gly	Tyr	355	360	365	
Gly	Tyr	Ala	Cys	Arg	Pro	Gly	Thr	Gln	Ser	Lys	Asp	Asp	Arg	Pro	Val	370	375	380	
Ser	Asp	Ile	Gly	Trp	Glu	Leu	Tyr	Pro	Glu	Gly	Met	Tyr	Asp	Ser	Ile	385	390	395	400
Val	Glu	Ala	His	Lys	Tyr	Gly	Val	Pro	Val	Tyr	Val	Thr	Glu	Asn	Gly	405	410	415	
Ile	Ala	Asp	Ser	Lys	Asp	Ile	Leu	Arg	Pro	Tyr	Tyr	Ile	Ala	Ser	His	420	425	430	
Ile	Lys	Met	Ile	Glu	Lys	Ala	Phe	Glu	Asp	Gly	Tyr	Glu	Val	Lys	Gly	435	440	445	
Tyr	Phe	His	Trp	Ala	Leu	Thr	Asp	Asn	Phe	Glu	Trp	Ala	Leu	Gly	Phe	450	455	460	
Arg	Met	Arg	Phe	Gly	Leu	Tyr	Glu	Val	Asn	Leu	Ile	Thr	Lys	Glu	Arg	465	470	475	480
Ile	Pro	Arg	Glu	Lys	Ser	Val	Ser	Ile	Phe	Arg	Glu	Ile	Val	Ala	Asn	485	490	495	
Asn	Gly	Val	Thr	Lys	Lys	Ile	Glu	Glu	Glu	Leu	Leu	Arg	Gly			500	505	510	

<210> 7

<211> 472

<212> PRT

<213> *Pyrococcus furiosus*

<400> 7

Met	Lys	Phe	Pro	Lys	Met	Phe	Met	Phe	Gly	Tyr	Ser	Trp	Ser	Gly	Pro
1				5					10					15	
Gln	Phe	Glu	Met	Gly	Leu	Pro	Gly	Ser	Glu	Val	Glu	Ser	Asp	Trp	Trp
			20					25					30		
Val	Trp	Val	His	Asp	Lys	Glu	Asn	Ile	Ala	Ser	Gly	Leu	Val	Ser	Gly
		35					40					45			
Asp	Leu	Pro	Glu	Asn	Gly	Pro	Ala	Tyr	Trp	His	Ile	Tyr	Lys	Gln	Asp
	50					55					60				
His	Asp	Ile	Ala	Glu	Lys	Leu	Gly	Met	Asp	Cys	Ile	Arg	Gly	Gly	Ile
65					70					75					80
Glu	Trp	Ala	Arg	Ile	Phe	Pro	Lys	Pro	Thr	Phe	Asp	Val	Lys	Val	Asp
				85					90					95	
Val	Glu	Lys	Asp	Glu	Glu	Gly	Asn	Ile	Ile	Ser	Val	Asp	Val	Pro	Glu
			100					105					110		
Ser	Thr	Ile	Lys	Glu	Leu	Glu	Lys	Ile	Ala	Asn	Met	Glu	Ala	Leu	Glu
		115					120					125			
His	Tyr	Arg	Lys	Ile	Tyr	Ser	Asp	Trp	Lys	Glu	Pro	Gly	Lys	Thr	Phe
	130					135					140				
Ile	Leu	Asn	Leu	Tyr	His	Trp	Pro	Leu	Pro	Leu	Trp	Ile	His	Asp	Pro
145					150					155					160
Ile	Ala	Val	Arg	Lys	Leu	Gly	Pro	Asp	Arg	Ala	Pro	Ala	Gly	Trp	Leu
				165					170					175	
Asp	Glu	Lys	Thr	Val	Val	Glu	Phe	Val	Lys	Phe	Ala	Ala	Phe	Val	Ala
			180					185					190		
Tyr	His	Leu	Asp	Asp	Leu	Val	Asp	Met	Trp	Ser	Thr	Met	Met	Glu	Pro
		195					200					205			
Met	Val	Val	Tyr	Asn	Gln	Gly	Tyr	Ile	Asn	Leu	Arg	Ser	Gly	Phe	Pro
	210					215					220				
Pro	Gly	Tyr	Leu	Ser	Phe	Glu	Ala	Ala	Glu	Lys	Ala	Lys	Phe	Asn	Leu
225					230					235					240
Ile	Gln	Ala	His	Ile	Gly	Ala	Tyr	Asp	Ala	Ile	Lys	Glu	Tyr	Ser	Glu
			245						250					255	
Lys	Ser	Val	Gly	Val	Ile	Tyr	Ala	Phe	Ala	Trp	His	Asp	Pro	Leu	Ala
			260					265					270		
Glu	Glu	Tyr	Lys	Asp	Glu	Val	Glu	Glu	Ile	Arg	Lys	Lys	Asp	Tyr	Glu
		275					280					285			
Phe	Val	Thr	Ile	Leu	His	Ser	Lys	Gly	Lys	Leu	Asp	Trp	Ile	Gly	Met
	290					295					300				
Asn	Tyr	Tyr	Ser	Arg	Leu	Val	Tyr	Gly	Ala	Lys	Asp	Gly	His	Leu	Val
305					310					315					320
Pro	Leu	Pro	Gly	Tyr	Gly	Phe	Met	Ser	Glu	Arg	Gly	Gly	Phe	Ala	Lys
			325						330				335		
Ser	Gly	Arg	Pro	Ala	Ser	Asp	Phe	Gly	Trp	Glu	Met	Tyr	Pro	Glu	Gly
			340					345					350		
Leu	Glu	Asn	Leu	Leu	Lys	Tyr	Leu	Asn	Asn	Ala	Tyr	Glu	Leu	Pro	Met
		355					360					365			
Ile	Ile	Thr	Glu	Asn	Gly	Met	Ala	Asp	Ala	Ala	Asp	Arg	Tyr	Arg	Pro
	370					375					380				
His	Tyr	Leu	Val	Ser	His	Leu	Lys	Ala	Val	Tyr	Asn	Ala	Met	Lys	Glu
385					390					395					400
Gly	Ala	Asp	Val	Arg	Gly	Tyr	Leu	His	Trp	Ser	Leu	Thr	Asp	Asn	Tyr
			405						410				415		
Glu	Trp	Ala	Gln	Gly	Phe	Arg	Met	Arg	Phe	Gly	Leu	Val	Tyr	Val	Asp
			420					425					430		
Phe	Glu	Thr	Lys	Lys	Arg	Tyr	Leu	Arg	Pro	Ser	Ala	Leu	Val	Phe	Arg
		435					440					445			
Glu	Ile	Ala	Thr	Gln	Lys	Glu	Ile	Pro	Glu	Glu	Leu	Ala	His	Leu	Ala
	450					455					460				
Asp	Leu	Lys	Phe	Val	Thr	Arg	Lys								

465

470

<210> 8

<211> 489

<212> PRT

<213> Sulfolobus solfataricus

<400> 8

Met Tyr Ser Phe Pro Asn Ser Phe Arg Phe Gly Trp Ser Gln Ala Gly
 1 5 10 15
 Phe Gln Ser Glu Met Gly Thr Pro Gly Ser Glu Asp Pro Asn Thr Asp
 20 25 30
 Trp Tyr Lys Trp Val His Asp Pro Glu Asn Met Ala Ala Gly Leu Val
 35 40 45
 Ser Gly Asp Leu Pro Glu Asn Gly Pro Gly Tyr Trp Gly Met Tyr Lys
 50 55 60
 Thr Phe His Asp Asn Ala Gln Lys Met Gly Leu Lys Ile Ala Arg Leu
 65 70 75 80
 Asn Val Glu Trp Ser Arg Ile Phe Pro Asn Pro Leu Pro Arg Pro Gln
 85 90 95
 Asn Phe Asp Glu Ser Lys Gln Asp Val Thr Glu Val Glu Ile Asn Glu
 100 105 110
 Asn Glu Leu Lys Arg Leu Asp Glu Tyr Ala Asn Lys Asp Ala Leu Asn
 115 120 125
 His Tyr Arg Glu Ile Phe Lys Asp Leu Lys Ser Pro Gly Leu Tyr Phe
 130 135 140
 Ile Leu Asn Met Tyr His Trp Pro Leu Pro Leu Trp Leu His Asp Pro
 145 150 155 160
 Ile Arg Val Arg Arg Gly Asp Phe Thr Gly Pro Ser Gly Trp Leu Ser
 165 170 175
 Thr Arg Thr Val Tyr Glu Phe Ala Arg Phe Ser Ala Tyr Ile Ala Trp
 180 185 190
 Lys Phe Asp Asp Leu Val Asp Glu Tyr Ser Thr Met Met Glu Pro Met
 195 200 205
 Val Val Gly Gly Leu Gly Tyr Val Gly Val Lys Ser Gly Phe Pro Pro
 210 215 220
 Gly Tyr Leu Ser Phe Glu Leu Ser Arg Arg His Met Tyr Asn Ile Ile
 225 230 235 240
 Gln Ala His Ala Arg Ala Tyr Asp Gly Ile Lys Ser Val Ser Lys Lys
 245 250 255
 Pro Val Gly Ile Ile Tyr Ala Asn Ser Ser Phe Gln Pro Leu Thr Asp
 260 265 270
 Lys Asp Met Glu Ala Val Glu Met Ala Glu Asn Asp Asn Arg Trp Trp
 275 280 285
 Phe Phe Asp Ala Ile Ile Arg Gly Glu Ile Thr Arg Gly Asn Glu Lys
 290 295 300
 Ile Val Arg Asp Asp Leu Lys Gly Arg Leu Asp Trp Ile Gly Met Asn
 305 310 315 320
 Tyr Tyr Thr Arg Thr Val Val Lys Arg Thr Glu Lys Gly Tyr Val Ser
 325 330 335
 Leu Gly Gly Tyr Gly His Gly Cys Glu Arg Asn Ser Val Ser Leu Ala
 340 345 350
 Gly Leu Pro Thr Ser Asp Phe Gly Trp Glu Phe Phe Pro Glu Gly Leu
 355 360 365
 Tyr Asp Val Leu Thr Lys Tyr Trp Asn Arg Tyr His Leu Tyr Met Tyr
 370 375 380
 Val Thr Glu Asn Gly Ile Ala Asp Asp Ala Asp Tyr Gln Arg Pro Tyr
 385 390 395 400
 Tyr Leu Val Ser His Val Tyr Gln Val His Arg Ala Ile Asn Ser Gly
 405 410 415
 Ala Asp Val Arg Gly Tyr Leu His Trp Ser Leu Ala Asp Asn Tyr Glu


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      420              425              430
Trp Ala Ser Gly Phe Ser Met Arg Phe Gly Leu Leu Phe Val Asp Tyr
      435              440              445
Asn Thr Lys Arg Leu Tyr Trp Arg Pro Ser Ala Leu Val Tyr Arg Glu
      450              455              460
Ile Ala Thr Asn Cys Ala Ile Thr Asp Glu Ile Glu His Leu Asn Ser
      465              470              475              480
Val Pro Pro Val Lys Pro Leu Arg His
      485

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<210> 9
<211> 285
<212> PRT
<213> Artificial Sequence

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<220>
<223> Consensus

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<400> 9
Met Phe Pro Glu Phe Gly Gln Ser Gly Phe Gln Phe Glu Met Gly Pro
 1              5              10              15
Asp Asp Trp Trp Trp Val Asp Asn Ile Gly Leu Val Ser Gly Asp Leu
      20              25              30
Pro Glu Gly Asn Trp Glu Leu Tyr Asp His Ala Lys Leu Gly Leu Asn
      35              40              45
Ala Tyr Arg Ile Glu Trp Ser Arg Ile Phe Pro Pro Thr Val Glu Ile
      50              55              60
Val Glu Leu Glu Leu Ala Asn Ala His Tyr Arg Ile Leu Lys Pro Gly
      65              70              75              80
Thr Ile Val Asn Leu His Thr Leu Pro Asp Trp His Asp Pro Ile Arg
      85              90              95
Gly Trp Leu Glu Arg Thr Val Glu Phe Ala Lys Tyr Ala Ala Tyr Val
      100              105              110
Ala Lys Phe Asp Asp Val Asp Trp Ser Thr Phe Asn Glu Pro Met Val
      115              120              125
Val Leu Gly Tyr Leu Tyr Ser Gly Phe Pro Pro Gly Leu Ser Pro Glu
      130              135              140
Ala Ala Lys Asn Ile Ala His Ala Ala Tyr Asp Ile Lys Ser Lys Pro
      145              150              155              160
Val Gly Ile Ile Tyr Asn Asp Pro Lys Asp Ala Ala Glu Phe Glu Ala
      165              170              175
Ile Gly Glu Pro Asp Trp Ile Gly Met Asn Tyr Tyr Thr Arg Val Val
      180              185              190
Glu Leu Pro Gly Tyr Gly Leu Ser Pro Ser Asp Phe Gly Trp Glu Tyr
      195              200              205
Arg Glu Gly Leu Tyr Asp Leu Ala Tyr Pro Tyr Ile Thr Glu Asn Gly
      210              215              220
Thr Ala Asp Asp Pro Pro Tyr Ile Ser His Val Lys Ala Ile Glu Gly
      225              230              235              240
Asp Val Pro Gly Tyr Phe His Trp Ser Leu Thr Asp Asn Tyr Glu Trp
      245              250              255
Ala Gly Glu Met Arg Glu Gly Leu Glu Val Asp Thr Lys Glu Arg Pro
      260              265              270
Arg Ser Ala Val Tyr Arg Glu Ile Ala Ile Glu Leu Arg
      275              280              285

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